

TCTAGACTGGACAGCATCCACAAGAGAAGCACCTAGAAGGAGAATTTTCCCCAGCAGCTTGCTCAGGACCC
TGCAGGAGCCGCAGCTGGGACTGGACCTGCTGTTAACCATGAACTCTTCCTGCTGCCTGTCTTCTGTTTCT
CCGATGCTGCCTAACCTCTCTGAGCACCCCTGCAGCCCCCTCTGCCAGCAACCGGAGCGGCAGTGGGTTCTG
TGAGCAGGTCTTCATCAAGCCGGAGGTCTTCCTGGCTCTGGGCATCGTCAGTCTGATGGAAAACATCCTGG
TGATCCTGGCTGTGGTCAGGAATGGCAACCTGCACTCTCCCATGTACTTCTTCCTGTGCAGCCTGGCTGCA
GCCGACATGCTGGTGAGCCTGTCCAACCTCCCTGGAGACCATCATGATCGCCGTGATCAACAGCGACTCCCT
GACCTTGGAGGACCAGTTTATCCAGCACATGGATAATATCTTCGACTCTATGATTTGCATCTCCCTGGTGG
CCTCCATCTGCAACCTCCTGGCCATTGCCATCGACAGGTACGTCACCATCTTCTATGCCCTTCGGTACCAC
AGCATCATGACAGTTAGGAAAGCCCTCACCTTGATCGGGGTCATCTGGGTCTGCTGCGGCATCTGCGGCGT
GATGTTTCATCATCTACTCCGAGAGCAAGATGGTCATCGTGTGTCTCATCACCATGTTCTTCGCCATGGTGC
TCCTCATGGGCACCCATATATACCATGTTCCTCTTCGCCAGGCTCCACGTCCAGCGCATCGCAGTGCTG
CCCCCTGCTGGCGTGGTGGCCCCACAGCAGCACTCCTGCATGAAGGGGGCTGTACCATCACTATCCTGCT
GGGTGTTTTTCATCTTCTGCTGGGCGCCTTTCTTCCTCCACCTGGTCTCATCATCACCCTGCCCCACCAATC
CCTACTGCATCTGCTACACGGCCCATTTCAACACCTACCTGGTTCTCATCATGTGCAACTCCGTATCGAC
CCCCTCATCTACGCCCTCCGCAGCCTGGAGCTGCGCAACACGTTCAAGGAGATTCTCTGCGGCTGCAACAG
CATGAACTTGGGCTAGGATGCCCCGTGGAGGTGTTCACATCCAGCCAAGAGACAAAAACAACGCTCAGACG
GGACGTAAGGGGTGTAGGAGCTGGAAGTGTGCTTGGCTTCGTCTGTAAGCTCGTGGCCCTTTGCAGACG
GGACACGGCGTAGGATGGGCTGTCTGTGAGGATCTGTGTGTGGGTAAGTCAGTTTGATCTAGCACATAGCC
TGGAGAATCAGGCAAAGCAGCCCTGAGTGTATCTGTGTTTATTGCTAGGCACCCAGGGTTTGTGGCCCC
TGCTTGCTTATTGGCTTTGTACCAGTAAGTGTGCTTCAAGCCAACCAGACCGGAGGGCTCTCGTGAGCAGA
AAGAGTGTCTAGACTTCCGGCAAGCATCCTGGCTCACAGCGGCCACCTCCTGACCACTACCGGGAGAGCTT
TGCACATATTCTGTGGGAGATTGAGTGAAGCCCTGAAAAACAATGTGATATTTGCTGCTCCCTTCCAGAACT
TACATCTGTGCCAGCCTCCCCGAACCCCTGCACAGAGACATGACCCCTTCTCCCTGTGCCGTTGTATGG
TTGTTATTATTGTTGGAGTTTGTTCGTTAAAAATCTAAGCTT (SEQ ID NO:1)

MNSSCCLSSVSPMLPNLSEHPAAPPASNRSGSGFCEQVFIKPEVFLALGIVSLMENILVILAVVRNGLHS
PMYFFLCSLAAADMLVSLSNSLETIMIAVINSDSLTLQFIQHMDNIFDSMICISLVASICNLLAIAIDR
YVTIFYALRYHSIMTVRKALTLIGVIWVCCGICGVMFIYSESKMVIVCLITMFFAMVLLMGTLYIHMFLF
ARLHVQRIAVLPPAGVVAPQQHSCMKGAVTITILLGVFIFCWAPFFLHLVLIITCPTNPYCICYTAHFNTY
LVLIMCNSVIDPLIYAFRSLELRNTFKEILCGCNSMNLG (SEQ ID NO:2)

FIGURE 1

Underlined = deleted in targeting construct

Bold = sequence flanking Neo insert in targeting construct

TCTAGACTGGACAGCATCCACAAGAGAAGCACCTAGAAGGAGAATTTTCCCCAGCAGCTT
GCTCAGGACCCCTGCAGGAGCCGCAGCTGGGACTGGACCTGCTGTTAACCATGAACCTTTC
CTGCTGCCTGTCTTCTGTTTCTCCGATGCTGCCTAACCTCTCTGAGCACCCCTGCAGCCCC
TCCTGCCAGCAACCGGAGCGGCAGTGGGTTCTGTGAGCAGGTCTTCATCAAGCCGGAGGT
CTTCTGGCTCTGGGCATCGTCAGTCTGATGGAAAACATCCTGGTGATCCTGGCTGTGGT
CAGGAATGGCAACCTGCACTCTCCCATGTACTTCTTCCTGTGCAGCCTGGCTGCAGCCGA
CATGCTGGTGAGCCTGTCCAACCTCCCTGGAGACCATCATGATCGCCGTGATCAACAGCGA
CTCCCTGACCTTGGAGGACCAGTTTATCCAGCACATGGATAATATCTTCGACTCTATGAT
TTGCATCTCCCTGGTGGCCTCCATCTGCAACCTCCTGGCCATTGGCCATCGACAGGTACGT
CACCATCTTCTATGCCCTTCGGTACCACAGCATCATGACAGTTAGGAAAGCCCTCACCTT
GATCGGGGTCTCTGGGTCTGCTGCGGCATCTGCGGCGTGATGTTTCATCATCTACTCCGA
GAGCAAGATGGTCATCGTGTGTCTCATCACCATGTTCTTCGCCATGGTGCTCCTCATGGG
CACCCTATATATCCACATGTTCTCTTCGCCAGGCTCCACGTCCAGCGCATCGCAGTGCT
GCCCCCTGCTGGCGTGGTGGCCCCACAGCAGCACTCCTGCATGAAGGGGGCTGTCACCAT
CACTATCCTGCTGGGTGTTTTTCATCTTCTGCTGGGCGCCTTTCTTCCTCCACCTGGTCTT
CATCATCACCTGCCCCACCAATCCCTACTGCATCTGCTACACGGCCCATTTCAACACCTA
CCTGGTTCTCATCATGTGCAACTCCGTCTGACCCCCCTCATCTACGCCTTCCGCAGCCT
GGAGCTGCGCAACACGTTCAAGGAGATTCTCTGCGGCTGCAACAGCATGAACCTGGGCTA
GGATGCCCGTGGAGGTGTTCCACATCCAGCCAAGAGACAAAAACAACGCTCAGACGGGAC
GTAAAAGGGTGTAGGAGCTGGAAGTGTGCTTGGCTTCGTCTGTAAGCTCGTGGCCCTTT
GCAGACGGGACACGGCGTAGGATGGGCTGTCTGTGAGGATCTGTGTGTGGGTAAGTCAGT
TTGATCTAGCACATAGCCTGGAAGAATCAGGCAAAGCAGCCCTGAGTGTCATCTGTGTTC
ATTGCTAGGCACCCAGGGTTTGTGGCCCCCTGCCTGCTTATTGGCTTTGTACCAGTAACCTG
TGCTTCAAGCCAACCAGACCGGAGGGCTCTCGTGAGCAGAAAGAGTGCTTAGACTTCCGG
CAAGCATCCTGGCTCACAGCGGCCACCTCCTGACCACTACCGGGAGAGCTTTGCACATAT
TCTGTGGGAGATTGAGTGAAGCCCTGAAAACAATGTGATATTTGCTGCTCCCTTCCAGAA
CTTACATCTGTGCCAGCCTCCCCGAACCCCTGCACAGAGACATGACCCCTTCTCCCTGT
GCCGTTGTCATGGTTGTTATTATTGTTGGAGTTTGTTCGTTAAAATCTAAGCTT

FIGURE 2A

Gene Sequence
Structure *

296 bp

Sequence Deleted

519 bp

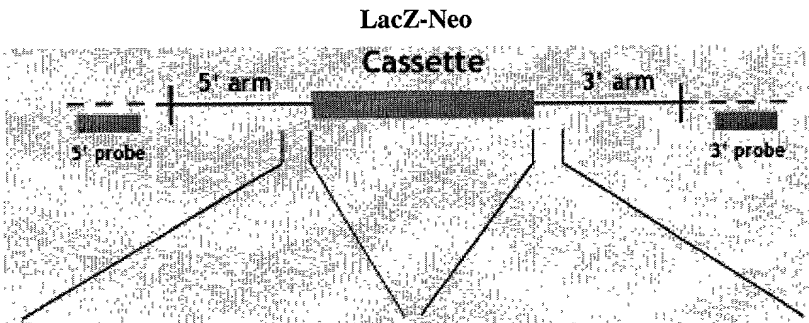
Size of CDS: 1675 bp



Targeting Vector* (genomic sequence)

Construct Number: 2787

Arm Length:
5': 1.6 kb
3': 4 kb



* Not drawn to scale

<p>5' >ACCTGCTGTTAACCATGAACT CTTCCTGCTGCCTGTCTTCTGTTT CTCCGATGCTGCCTAACCTCTCTG AGCACCCCTGCAGCCCCCTCCTGCCA GCAACCGGAGCGGCAGTGGGTTCT GTGAGCAGGTCTTCATCAAGCCGG AGGTCTTCCTGGCTCTGGGCATCG TCAGTCTGATGGAAAACATCCTGG TGATCCTGGCT<3' (SEQ ID NO:3)</p>	<p>5' >CATTGCCATCGACAGGTACGT CACCATCTTCTATGCCCTTCGGTA CCACAGCATCATGACAGTGAGGAA AGCCCTCACCTTGATCGGGGTCAT CTGGGTCTGCTGCGGCATCTGCGG CGTGATGTTTCATCATCTACTCCGA GAGCAAGATGGTCATCGTGTGTCT CATCACCATGTTCTTCGCCATGGT GCTCCTCATGG<3' (SEQ ID NO:4)</p>
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FIGURE 2B